IN THE SPECIFICATION:

Please replace the paragraph at page 15, line 21 with the following paragraph:

--Several class switch regions (S regions) have been characterized, including the murine Sμ, Sε, Sα, $S\gamma_3$, $S\gamma_1$, $S\gamma_{2a}$ and $S\gamma_{2b}$ switch regions and human Sμ and Sγ switch regions (Mills et al., (1995), *supra.*) For example, the murine Sμ region is about 3 kb and can be divided into a 3' region with sequences $[(GAGCT)_nGGGGT]_m$, $[(SEQ\ ID\ NO:109)_n SEQ\ ID\ NO:110]_m$ wherein n=1-7 and m=150 (Nikaido et al., Nature 292:845-848 (1981)), and a 5' region in which these two pentamers are interspersed with the following heptamer sequence: (C/T)AGGTTG (SEQ ID NO:111) (Marcu et al, Nature 298:87-89 (1982)). The human Sμ sequence is different in that the heptamer sequence is distributed throughout the region (Takahashi et al., Cell 29:671-679 (1982); Mills et al. (1995) *supra*). All S sequences contain multiple copies of the pentameric sequences GAGCT (SEQ ID NO:109) and GGGGT (SEQ ID NO:110), and the pentamers ACCAG (SEQ ID NO:111), GCAGC (SEQ ID NO:112), and TGAGC (SEQ ID NO:113) are also commonly found in S regions (Gritzmacher, Crit. Rev. Immunol. 9:173-299 (1989)). In addition, the foregoing heptameric repeat is also commonly found in native S regions. All these regions/repeats, and similar regions from other murine or human S regions will be referred to as "GC rich" regions or repeats.--

Please replace the paragraph at page 43, line 31 with the following paragraph:

--One characteristic feature of Ig class switch recombination is that deletional recombination between two involved S regions is region specific but site non-specific; i.e. it falls in the category of "illegitimate" recombination (Dunnick et al., Nucleic Acids Res. 21:365-372 (1993)). To show that the recombination sites employed following nuclear extract-driven recombination demonstrate this feature, we sequenced the recombination junctures of recombined clones. Thirty-two randomly selected colonies that hybridized to both Sμ and Sε probes from the *in vitro* recombination assay and 17 colonies derived from direct PCR amplification were sequenced. The breakpoints were defined by alignment of the clone sequences with the Sμ and Sε sequences in plasmid p77D3.11. The sequences around the recombination junctions from 10 clones derived from recombination assay and 10 clones from PCR amplification are shown in Figures 13A and 13B, respectively. The homology between Sμ and Sε in these sequence identified clones from both recombination assay and PCR assay varies from a homology of 15 (clone SR.23-10) nucleotides to 0 (e.g., clones

R5.22-10, R5.29-22, SR6.16-13). Clones that contained unmatched sequences in the breakpoint to both Sμ and Sε are also presented (clones R6.4-39, SR9.24-20, and SR28-27). Thus, although clones derived from the *in vitro* recombination assay often share a short stretch of homology for Sμ and Sε in the junctional sites as seen in *in vivo* CSR, homology between Sμ and Sε was not required for switch-region DNA recombination in our system. The frequently observed short homologous stretches between Sμ and Sε at the recombination junctions likely reflect the internal features of the Sμ and Sε constructs used to make p77D3.11, with its tandemly repetitive sequences GGGCT (SEQ ID NO:114), GGGGT (SEQ ID NO:110), and GAGCT (SEQ ID NO:109) densely distributed throughout the Sμ and Sε segments.--